SEQUENCE LISTING

<110> Keener, William K.
Ward, Thomas E.

<120> SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN IMMUNODEFICIENCY VIRUS

<130> LIT-PI-529

<140> US 09/785,921

<141> 2001-02-15

<160> 17

<210> 1

<211> 1698

<212> DNA

<213> Ricinus communis

<400> 1

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tgg tct ttc aca tta gag gat aac aac ata ttc ccc aaa caa tac 90
Trp Ser Phe Thr Leu Glu Asp Asn Asn Ile Phe Pro Lys Gln Tyr
                -5                  1                   5

cca att ata aac ttt acc aca gcg ggt gcc act gtg caa agc tac 135
Pro Ile Ile Asn Phe Thr Thr Ala Gly Ala Thr Val Gln Ser Tyr
            10                  15                  20

aca aac ttt atc aga gct gtt cgc ggt cgt tta aca act gga gct 180
Thr Asn Phe Ile Arg Ala Val Arg Gly Arg Leu Thr Thr Gly Ala
            25                  30                  35

gat gtg aga cat gat ata cca gtg ttg cca aac aga gtt ggt ttg 225
Asp Val Arg His Asp Ile Pro Val Leu Pro Asn Arg Val Gly Leu
            40                  45                  50

cct ata aac caa cgg ttt att tta gtt gaa ctc tca aat cat gca 270
Pro Ile Asn Gln Arg Phe Ile Leu Val Glu Leu Ser Asn His Ala
            55                  60                  65
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gag ctt tct gtt aca tta gcc ctg gat gtc acc aat gca tat gtg 315
Glu Leu Ser Val Thr Leu Ala Leu Asp Val Thr Asn Ala Tyr Val
            70                  75                  80

gtc ggc tac cgt gct gga aat agc gca tat ttc ttt cat cct gac 360
Val Gly Tyr Arg Ala Gly Asn Ser Ala Tyr Phe Phe His Pro Asp
            85                  90                  95

aat cag gaa gat gca gaa gca atc act cat ctt ttc act gat gtt 405
Asn Gln Glu Asp Ala Glu Ala Ile Thr His Leu Phe Thr Asp Val
           100                 105                 110

caa aat cga tat aca ttc gcc ttt ggt ggt aat tat gat aga ctt 450
Gln Asn Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp Arg Leu
           115                 120                 125

gaa caa ctt gct ggt aat ctg aga gaa aat atc gag ttg gga aat 495
Glu Gln Leu Ala Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly Asn
           130                 135                 140

ggt cca cta gag gag gct atc tca gcg ctt tat tat tac agt act 540
Gly Pro Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr
           145                 150                 155

ggt ggc act cag ctt cca act ctg gct cgt tcc ttt ata att tgc 585
Gly Gly Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys
           160                 165                 170

atc caa atg att tca gaa gca gca aga ttc caa tat att gag gga 630
Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly
           175                 180                 185

gaa atg cgc acg aga att agg tac aac cgg aga tct gca cca gat 675
Glu Met Arg Thr Arg Ile Arg Tyr Asn Arg Arg Ser Ala Pro Asp
           190                 195                 200

cct agc gta att aca ctt gag aat agt tgg ggg aga ctt tcc act 720
Pro Ser Val Ile Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr
           205                 210                 215

gca att caa gag tct aac caa gga gcc ttt gct agt cca att caa 765
Ala Ile Gln Glu Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile Gln
           220                 225                 230

ctg caa aga cgt aat ggt tcc aaa ttc agt gtg tac gat gtg agt 810
Leu Gln Arg Arg Asn Gly Ser Lys Phe Ser Val Tyr Asp Val Ser
           235                 240                 245
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ata tta atc cct atc ata gct ctc atg gtg tat aga tgc gca cct 855
Ile Leu Ile Pro Ile Ile Ala Leu Met Val Tyr Arg Cys Ala Pro
            250                 255                 260

cca cca tcg tca cag ttt tct ttg ctt ata agg cca gtg gta cca 900
Pro Pro Ser Ser Gln Phe Ser Leu Leu Ile Arg Pro Val Val Pro
            265                 270                 275

aat ttt aat gct gat gtt tgt atg gat cct gag ccc ata gtg cgt 945
Asn Phe Asn Ala Asp Val Cys Met Asp Pro Glu Pro Ile Val Arg
            280                 285                 290

atc gta ggt cga aat ggt cta tgt gtt gat gtt agg gat gga aga 990
Ile Val Gly Arg Asn Gly Leu Cys Val Asp Val Arg Asp Gly Arg
            295                 300                 305

ttc cac aac gga aac gca ata cag ttg tgg cca tgc aag tct aat 1035
Phe His Asn Gly Asn Ala Ile Gln Leu Trp Pro Cys Lys Ser Asn
            310                 315                 320

aca gat gca aat cag ctc tgg act ttg aaa aga gac aat act att 1080
Thr Asp Ala Asn Gln Leu Trp Thr Leu Lys Arg Asp Asn Thr Ile
            325                 330                 335

cga tct aat gga aag tgt tta act act tac ggg tac agt ccg gga 1125
Arg Ser Asn Gly Lys Cys Leu Thr Thr Tyr Gly Tyr Ser Pro Gly
            340                 345                 350

gtc tat gtg atg atc tat gat tgc aat act gct gca act gat gcc 1170
Val Tyr Val Met Ile Tyr Asp Cys Asn Thr Ala Ala Thr Asp Ala
            355                 360                 365

acc cgc tgg caa ata tgg gat aat gga acc atc ata aat ccc aga 1215
Thr Arg Trp Gln Ile Trp Asp Asn Gly Thr Ile Ile Asn Pro Arg
            370                 375                 380

tct agt cta gtt tta gca gcg aca tca ggg aac agt ggt acc aca 1260
Ser Ser Leu Val Leu Ala Ala Thr Ser Gly Asn Ser Gly Thr Thr
            385                 390                 395

ctt acg gtg caa acc aac att tat gcc gtt agt caa ggt tgg ctt 1305
Leu Thr Val Gln Thr Asn Ile Tyr Ala Val Ser Gln Gly Trp Leu
            400                 405                 410

cct act aat aat aca caa cct ttt gtt aca acc att gtt ggg cta 1350
Pro Thr Asn Asn Thr Gln Pro Phe Val Thr Thr Ile Val Gly Leu
            415                 420                 425
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tat ggt ctg tgc ttg caa gca aat agt gga caa gta tgg ata gag 1395
Tyr Gly Leu Cys Leu Gln Ala Asn Ser Gly Gln Val Trp Ile Glu
430 435 440

gac tgt agc agt gaa aag gct gaa caa cag tgg gct ctt tat gca 1440
Asp Cys Ser Ser Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala
445 450 455

gat ggt tca ata cgt cct cag caa aac cga gat aat tgc ctt aca 1485
Asp Gly Ser Ile Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr
460 465 470

agt gat tct aat ata cgg gaa aca gtt gtt aag atc ctc tct tgt 1530
Ser Asp Ser Asn Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys
475 480 485

ggc cct gca tcc tct ggc caa cga tgg atg ttc aag aat gat gga 1575
Gly Pro Ala Ser Ser Gly Gln Arg Trp Met Phe Lys Asn Asp Gly
490 495 500

acc att tta aat ttg tat agt gga ttg gtg tta gat gtg agg cga 1620
Thr Ile Leu Asn Leu Tyr Ser Gly Leu Val Leu Asp Val Arg Arg
505 510 515

tcg gat ccg agc ctt aaa caa atc att ctt tac cct ctc cat ggt 1665
Ser Asp Pro Ser Leu Lys Gln Ile Ile Leu Tyr Pro Leu His Gly
520 525 530

gac cca aac caa ata tgg tta cca tta ttt tga 1698
Asp Pro Asn Gln Ile Trp Leu Pro Leu Phe
535 540

<210> 2

<211> 1731

<212> DNA

<213> Ricinus communis

<400> 2

atg aaa ccg gga gga aat act att gta ata tgg atg tat gca gtg 45
Met Lys Pro Gly Gly Asn Thr Ile Val Ile Trp Met Tyr Ala Val
-35 -30 -25

gca aca tgg ctt tgt ttt gga tcc acc tca ggg tgg tct ttc aca 90

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      Ala Thr Trp Leu Cys Phe Gly Ser Thr Ser Gly Trp Ser Phe Thr
      -20                 -15                 -10

      tta gag gat aac aac ata ttc ccc aaa caa tac cca att ata aac 135
      Leu Glu Asp Asn Asn Ile Phe Pro Lys Gln Tyr Pro Ile Ile Asn
 5    -5              -1   1                5                  10

      ttt acc aca gcg ggt gcc act gtg caa agc tac aca aac ttt atc 180
      Phe Thr Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile
                      15                  20                  25

      aga gct gtt cgc ggt cgt tta aca act gga gct gat gtg aga cat 225
10    Arg Ala Val Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His
                      30                  35                  40

      gaa ata cca gtg ttg cca aac aga gtt ggt ttg cct ata aac caa 270
      Glu Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile Asn Gln
                      45                  50                  55

15    cgg ttt att tta gtt gaa ctc tca aat cat gca gag ctt tct gtt 315
      Arg Phe Ile Leu Val Glu Leu Ser Asn His Ala Glu Leu Ser Val
                      60                  65                  70

      aca tta gcg ctg gat gtc acc aat gca tat gtg gtc ggc tac cgt 360
      Thr Leu Ala Leu Asp Val Thr Asn Ala Tyr Val Val Gly Tyr Arg
20                    75                  80                  85

      gct gga aat agc gca tat ttc ttt cat cct gac aat cag gaa gat 405
      Ala Gly Asn Ser Ala Tyr Phe Phe His Pro Asp Asn Gln Glu Asp
                      90                  95                  100

      gca gaa gca atc act cat ctt ttc act gat gtt caa aat cga tat 450
25    Ala Glu Ala Ile Thr His Leu Phe Thr Asp Val Gln Asn Arg Tyr
                      105                 110                 115

      aca ttc gcc ttt gga ggt aat tat gat aga ctt gaa caa ctt gct 495
      Thr Phe Ala Phe Gly Gly Asn Tyr Asp Arg Leu Glu Gln Leu Ala
                      120                 125                 130

30    ggt aat ctg aga gaa aat atc gag ttg gga aat ggt cca cta gag 540
      Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly Asn Gly Pro Leu Glu
                      135                 140                 145

      gag gct atc tca gcg ctt tat tat tac agt act ggt ggc act cag 585
      Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr Gly Gly Thr Gln
35                    150                 155                 160

      ctt cca act ctg gct cgt tcc ttt ata att tgc atc caa atg att 630
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Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys Ile Gln Met Ile
                165                 170                 175

tca gaa gca gca aga ttc caa tat att gag gga gaa atg cgc acg 675
Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly Glu Met Arg Thr
5               180                 185                 190

aga att agg tac aac cgg aga tct gca cca gat cct agc gta att 720
Arg Ile Arg Tyr Asn Arg Arg Ser Ala Pro Asp Pro Ser Val Ile
                195                 200                 205

aca ctt gag aat agt tgg ggg aga ctt tcc act gca att caa gag 765
10  Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala Ile Gln Glu
                210                 215                 220

tct aac caa gga gcc ttt gct agt cca att caa ctg caa aga cgt 810
Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile Gln Leu Gln Arg Arg
                225                 230                 235

15  aat ggt tcc aaa ttc agt gtg tac gat gtg agt ata tta atc cct 855
Asn Gly Ser Lys Phe Ser Val Tyr Asp Val Ser Ile Leu Ile Pro
                240                 245                 250

atc ata gct ctc atg gtg tat aga tgc gca cct cca cca tcg tca 900
Ile Ile Ala Leu Met Val Tyr Arg Cys Ala Pro Pro Pro Ser Ser
20              255                 260                 265

cag ttt tct ttg ctt ata agg cca gtg gta cca aat ttt aat gct 945
Gln Phe Ser Leu Leu Ile Arg Pro Val Val Pro Asn Phe Asn Ala
                270                 275                 280

gat gtt tgt atg gat cct gag ccc ata gtg cgt atc gta ggt cga 990
25  Asp Val Cys Met Asp Pro Glu Pro Ile Val Arg Ile Val Gly Arg
                285                 290                 295

aat ggt cta tgt gtt gat gtt agg gat gga aga ttc cac aac gga 1035
Asn Gly Leu Cys Val Asp Val Arg Asp Gly Arg Phe His Asn Gly
                300                 305                 310

30  aac gca ata cag ttg tgg cca tgc aag tct aat aca gat gca aat 1080
Asn Ala Ile Gln Leu Trp Pro Cys Lys Ser Asn Thr Asp Ala Asn
                315                 320                 325

cag ctc tgg act ttg aaa aga gac aat act att cga tct aat gga 1125
Gln Leu Trp Thr Leu Lys Arg Asp Asn Thr Ile Arg Ser Asn Gly
35              330                 335                 340

aag tgt tta act act tac ggg tac agt ccg gga gtc tat gtg atg 1170
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Lys Cys Leu Thr Thr Tyr Gly Tyr Ser Pro Gly Val Tyr Val Met
                345                 350                 355

atc tat gat tgc aat act gct gca act gat gcc acc cgc tgg caa 1215
Ile Tyr Asp Cys Asn Thr Ala Ala Thr Asp Ala Thr Arg Trp Gln
                360                 365                 370

ata tgg gat aat gga acc atc ata aat ccc aga tct agt cta gtt 1260
Ile Trp Asp Asn Gly Thr Ile Ile Asn Pro Arg Ser Ser Leu Val
                375                 380                 385

tta gca gcg aca tca ggg aac agt ggt acc aca ctt aca gtg caa 1305
Leu Ala Ala Thr Ser Gly Asn Ser Gly Thr Thr Leu Thr Val Gln
                390                 395                 400

acc aac att tat gcc gtt agt caa ggt tgg ctt cct act aat aat 1350
Thr Asn Ile Tyr Ala Val Ser Gln Gly Trp Leu Pro Thr Asn Asn
                405                 410                 415

aca caa cct ttt gtg aca acc att gtt ggg cta tat ggt ctg tgc 1395
Thr Gln Pro Phe Val Thr Thr Ile Val Gly Leu Tyr Gly Leu Cys
                420                 425                 430

ttg caa gca aat agt gga caa gta tgg ata gag gac tgt agc agt 1440
Leu Gln Ala Asn Ser Gly Gln Val Trp Ile Glu Asp Cys Ser Ser
                435                 440                 445

gaa aag gct gaa caa cag tgg gct ctt tat gca gat ggt tca ata 1485
Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala Asp Gly Ser Ile
                450                 455                 460

cgt cct cag caa aac cga gat aat tgc ctt aca agt gat tct aat 1530
Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr Ser Asp Ser Asn
                465                 470                 475

ata cgg gaa aca gtt gtc aag atc ctc tct tgt ggc cct gca tcc 1575
Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys Gly Pro Ala Ser
                480                 485                 490

tct ggc caa cga tgg atg ttc aag aat gat gga acc att tta aat 1620
Ser Gly Gln Arg Trp Met Phe Lys Asn Asp Gly Thr Ile Leu Asn
                495                 500                 505

ttg tat agt ggg ttg gtg tta gat gtg agg gca tcg gat ccg agc 1665
Leu Tyr Ser Gly Leu Val Leu Asp Val Arg Ala Ser Asp Pro Ser
                510                 515                 520

ctt aaa caa atc att ctt tac cct ctc cat ggt gac cca aac caa 1710
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Leu Lys Gln Ile Ile Leu Tyr Pro Leu His Gly Asp Pro Asn Gln
525 530 535

ata tgg tta cca tta ttt tga 1731
Ile Trp Leu Pro Leu Phe
540

<210> 3

<211> 1731

<212> DNA

<213> Ricinus communis

<400> 3

atg aaa ccg gga gga aat act att gta ata tgg atg tat gca gtg 45
Met Lys Pro Gly Gly Asn Thr Ile Val Ile Trp Met Tyr Ala Val
-35 -30 -25

gca aca tgg ctt tgt ttt gga tcc acc tca ggg tgg tct ttc aca 90
Ala Thr Trp Leu Cys Phe Gly Ser Thr Ser Gly Trp Ser Phe Thr
-20 -15 -10

tta gag gat aac aac ata ttc ccc aaa caa tac cca att ata aac 135
Leu Glu Asp Asn Asn Ile Phe Pro Lys Gln Tyr Pro Ile Ile Asn
-5 -1 1 5 10

ttt acc aca gcg ggt gcc act gtg caa agc tac aca aac ttt atc 180
Phe Thr Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn Phe Ile
15 20 25

aga gct gtt cgc ggt cgt tta aca act gga gct gat gtg aga cat 225
Arg Ala Val Arg Gly Arg Leu Thr Thr Gly Ala Asp Val Arg His
30 35 40

gaa ata cca gtg ttg cca aac aga gtt ggt ttg cct ata aac caa 270
Glu Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile Asn Gln
45 50 55

cgg ttt att tta gtt gaa ctc tca aat cat gca gag ctt tct gtt 315
Arg Phe Ile Leu Val Glu Leu Ser Asn His Ala Glu Leu Ser Val
60 65 70

aca tta gcg ctg gat gtc acc aat gca tat gtg gtc ggc tac cgt 360
Thr Leu Ala Leu Asp Val Thr Asn Ala Tyr Val Val Gly Tyr Arg

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                    75                  80                  85

gct gga aat agc gca tat ttc ttt cat cct gac aat cag gaa gat 405
Ala Gly Asn Ser Ala Tyr Phe Phe His Pro Asp Asn Gln Glu Asp
                    90                  95                  100

gca gaa gca atc act cat ctt ttc act gat gtt caa aat cga tat 450
Ala Glu Ala Ile Thr His Leu Phe Thr Asp Val Gln Asn Arg Tyr
                    105                 110                 115

aca ttc gcc ttt ggt ggt aat tat gat aga ctt gaa caa ctt gct 495
Thr Phe Ala Phe Gly Gly Asn Tyr Asp Arg Leu Glu Gln Leu Ala
                    120                 125                 130

ggt aat ctg aga gaa aat atc gag ttg gga aat ggt cca cta gag 540
Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly Asn Gly Pro Leu Glu
                    135                 140                 145

gag gct atc tca gcg ctt tat tat tac agt act ggt ggc act cag 585
Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr Gly Gly Thr Gln
                    150                 155                 160

ctt cca act ctg gct cgt tcc ttt ata att tgc atc caa atg att 630
Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys Ile Gln Met Ile
                    165                 170                 175

tca gaa gca gca aga ttc caa tat att gag gga gaa atg cgc acg 675
Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly Glu Met Arg Thr
                    180                 185                 190

aga att agg tac aac cgg aga tct gca cca gat cct agc gta att 720
Arg Ile Arg Tyr Asn Arg Arg Ser Ala Pro Asp Pro Ser Val Ile
                    195                 200                 205

aca ctt gag aat agt tgg ggg aga ctt tca act gca att caa gag 765
Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala Ile Gln Glu
                    210                 215                 220

tct aac caa gga gcc ttt gct agt cca att caa ctg caa aga cgt 810
Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile Gln Leu Gln Arg Arg
                    225                 230                 235

aat ggt tcc aaa ttc agt gtg tac gat gtg agt ata tta atc cct 855
Asn Gly Ser Lys Phe Ser Val Tyr Asp Val Ser Ile Leu Ile Pro
                    240                 245                 250

atc ata gct ctc atg gtg tat aga tgc gca cct cca cca tcg tca 900
Ile Ile Ala Leu Met Val Tyr Arg Cys Ala Pro Pro Pro Ser Ser
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                    255                 260                 265

     cag ttt tct ttg ctt ata agg cca gtg gta cca aat ttt aat gct 945
     Gln Phe Ser Leu Leu Ile Arg Pro Val Val Pro Asn Phe Asn Ala
                    270                 275                 280

     gat gtt tgt atg gat cct gag ccc ata gtg cgt atc gta ggt cga 990
     Asp Val Cys Met Asp Pro Glu Pro Ile Val Arg Ile Val Gly Arg
                    285                 290                 295

     aat ggt cta tgt gtt gat gtt agg gat gga aga ttc cac aac gga 1035
     Asn Gly Leu Cys Val Asp Val Arg Asp Gly Arg Phe His Asn Gly
                    300                 305                 310

     aac gca ata cag ttg tgg cca tgc aag tct aat aca gat gca aat 1080
     Asn Ala Ile Gln Leu Trp Pro Cys Lys Ser Asn Thr Asp Ala Asn
                    315                 320                 325

     cag ctc tgg act ttg aaa aga gac aat act att cga tct aat gga 1125
     Gln Leu Trp Thr Leu Lys Arg Asp Asn Thr Ile Arg Ser Asn Gly
                    330                 335                 340

     aag tgt tta act act tac ggg tac agt ccg gga gtc tat gtg atg 1170
     Lys Cys Leu Thr Thr Tyr Gly Tyr Ser Pro Gly Val Tyr Val Met
                    345                 350                 355

     atc tat gat tgc aat act gct gca act gat gcc acc cgc tgg caa 1215
     Ile Tyr Asp Cys Asn Thr Ala Ala Thr Asp Ala Thr Arg Trp Gln
                    360                 365                 370

     ata tgg gat aat gga acc atc ata aat ccc aga tct agt cta gtt 1260
     Ile Trp Asp Asn Gly Thr Ile Ile Asn Pro Arg Ser Ser Leu Val
                    375                 380                 385

     tta gca gcg aca tca ggg aac agt ggt acc aca ctt aca gtg caa 1305
     Leu Ala Ala Thr Ser Gly Asn Ser Gly Thr Thr Leu Thr Val Gln
                    390                 395                 400

     acc aac att tat gcc gtt agt caa ggt tgg ctt cct act aat aat 1350
     Thr Asn Ile Tyr Ala Val Ser Gln Gly Trp Leu Pro Thr Asn Asn
                    405                 410                 415

     aca caa cct ttt gtg aca acc att gtt ggg cta tat ggt ctg tgc 1395
     Thr Gln Pro Phe Val Thr Thr Ile Val Gly Leu Tyr Gly Leu Cys
                    420                 425                 430

     ttg caa gca aat agt gga caa gta tgg ata gag gac tgt agc agt 1440
     Leu Gln Ala Asn Ser Gly Gln Val Trp Ile Glu Asp Cys Ser Ser
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                    435                 440                 445

     gaa aag gct gaa caa cag tgg gct ctt tat gca gat ggt tca ata 1485
     Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala Asp Gly Ser Ile
                    450                 455                 460

     cgt cct cag caa aac cga gat aat tgc ctt aca agt gat tct aat 1530
     Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr Ser Asp Ser Asn
                    465                 470                 475

     ata cgg gaa aca gtt gtc aag atc ctc tct tgt ggc cct gca tcc 1575
     Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys Gly Pro Ala Ser
                    480                 485                 490

     tct ggc caa cga tgg atg ttc aag aat gat gga acc att tta aat 1620
     Ser Gly Gln Arg Trp Met Phe Lys Asn Asp Gly Thr Ile Leu Asn
                    495                 500                 505

     ttg tat agt ggg ttg gtg tta gat gtg agg gca tcg gat ccg agc 1665
     Leu Tyr Ser Gly Leu Val Leu Asp Val Arg Ala Ser Asp Pro Ser
                    510                 515                 520

     ctt aaa caa atc att ctt tac cct ctc cat ggt gac cca aac caa 1710
     Leu Lys Gln Ile Ile Leu Tyr Pro Leu His Gly Asp Pro Asn Gln
                    525                 530                 535

     ata tgg tta cca tta ttt tga 1731
     Ile Trp Leu Pro Leu Phe
                    540
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<210> 4

<211> 10

<212> PRT

<213> Human immunodeficiency virus

<400> 4

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Val Ser Gln Asn Tyr Pro Ile Val Gln Asn
 1               5                  10
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<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Encodes the modified proricin linker sequence of SEQ ID NO:4.

<400> 5

gtt tct caa aac tac cca att gtt caa aat 30
Val Ser Gln Asn Tyr Pro Ile Val Gln Asn
1 5 10

<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for amplifying the 5' portion of the preproricin gene and incorporating a SacI recognition site.

<400> 6

ctcgagctct gaaaccggga ggaaatact 29

<210> 7

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for amplifying the 5' portion of the preproricin gene, mutating the linker sequence, and incorporating a MfeI recognition site.

<400> 7

ttgaacaatt gggtagtttt gagaaacaaa ctgtgacgat ggtggaggtg 50

<210> 8

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for amplifying the 3' portion of the preproricin gene, mutating the linker sequence, and incorporating a MfeI recognition site.

<400> 8

ctacccaatt gttcaaaatt ttaatgctga tgtttgtatg g 41

<210> 9

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for amplifying the 3' portion of the preproricin gene and incorporating an XhoI recognition site.

<400> 9

ctcctcgagt ttaagccatc tattttcat 29

<210> 10

<211> 1805

<212> DNA

<213> Ricinus communis

<400> 10

ctcgagctct gaaaccggga ggaaatacta ttgtaatatg g atg tat 47

Met Tyr

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gca gtg gca aca tgg ctt tgt ttt gga tcc acc tca ggg tgg tct 92
Ala Val Ala Thr Trp Leu Cys Phe Gly Ser Thr Ser Gly Trp Ser
        -20                 -15                 -10

ttc aca tta gag gat aac aac ata ttc ccc aaa caa tac cca att 137
Phe Thr Leu Glu Asp Asn Asn Ile Phe Pro Lys Gln Tyr Pro Ile
        -5                   1                   5

ata aac ttt acc aca gcg ggt gcc act gtg caa agc tac aca aac 182
Ile Asn Phe Thr Thr Ala Gly Ala Thr Val Gln Ser Tyr Thr Asn
    10                  15                  20

ttt atc aga gct gtt cgc ggt cgt tta aca act gga gct gat gtg 227
Phe Ile Arg Ala Val Arg Gly Arg Leu Thr Thr Gly Ala Asp Val
    25                  30                  35

aga cat gaa ata cca gtg ttg cca aac aga gtt ggt ttg cct ata 272
Arg His Glu Ile Pro Val Leu Pro Asn Arg Val Gly Leu Pro Ile
    40                  45                  50

aac caa cgg ttt att tta gtt gaa ctc tca aat cat gca gag ctt 317
Asn Gln Arg Phe Ile Leu Val Glu Leu Ser Asn His Ala Glu Leu
    55                  60                  65

tct gtt aca tta gcg ctg gat gtc acc aat gca tat gtg gtc ggc 362
Ser Val Thr Leu Ala Leu Asp Val Thr Asn Ala Tyr Val Val Gly
    70                  75                  80

tac cgt gct gga aat agc gca tat ttc ttt cat cct gac aat cag 407
Tyr Arg Ala Gly Asn Ser Ala Tyr Phe Phe His Pro Asp Asn Gln
    85                  90                  95

gaa gat gca gaa gca atc act cat ctt ttc act gat gtt caa aat 452
Glu Asp Ala Glu Ala Ile Thr His Leu Phe Thr Asp Val Gln Asn
    100                 105                 110

cga tat aca ttc gcc ttt ggt ggt aat tat gat aga ctt gaa caa 497
Arg Tyr Thr Phe Ala Phe Gly Gly Asn Tyr Asp Arg Leu Glu Gln
    115                 120                 125

ctt gct ggt aat ctg aga gaa aat atc gag ttg gga aat ggt cca 542
Leu Ala Gly Asn Leu Arg Glu Asn Ile Glu Leu Gly Asn Gly Pro
    130                 135                 140

cta gag gag gct atc tca gcg ctt tat tat tac agt act ggt ggc 587
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Leu Glu Glu Ala Ile Ser Ala Leu Tyr Tyr Tyr Ser Thr Gly Gly
    145                 150                 155

act cag ctt cca act ctg gct cgt tcc ttt ata att tgc atc caa 632
Thr Gln Leu Pro Thr Leu Ala Arg Ser Phe Ile Ile Cys Ile Gln
    160                 165                 170

atg att tca gaa gca gca aga ttc caa tat att gag gga gaa atg 677
Met Ile Ser Glu Ala Ala Arg Phe Gln Tyr Ile Glu Gly Glu Met
    175                 180                 185

cgc acg aga att agg tac aac cgg aga tct gca cca gat cct agc 722
Arg Thr Arg Ile Arg Tyr Asn Arg Arg Ser Ala Pro Asp Pro Ser
    190                 195                 200

gta att aca ctt gag aat agt tgg ggg aga ctt tca act gca att 767
Val Ile Thr Leu Glu Asn Ser Trp Gly Arg Leu Ser Thr Ala Ile
    205                 210                 215

caa gag tct aac caa gga gcc ttt gct agt cca att caa ctg caa 812
Gln Glu Ser Asn Gln Gly Ala Phe Ala Ser Pro Ile Gln Leu Gln
    220                 225                 230

aga cgt aat ggt tcc aaa ttc agt gtg tac gat gtg agt ata tta 857
Arg Arg Asn Gly Ser Lys Phe Ser Val Tyr Asp Val Ser Ile Leu
    235                 240                 245

atc cct atc ata gct ctc atg gtg tat aga tgc gca cct cca cca 902
Ile Pro Ile Ile Ala Leu Met Val Tyr Arg Cys Ala Pro Pro Pro
    250                 255                 260

tcg tca cag ttt gtt tct caa aac tac cca att gtt caa aat ttt 947
Ser Ser Gln Phe Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Phe
    265                 270                 275

aat gct gat gtt tgt atg gat cct gag ccc ata gtg cgt atc gta 992
Asn Ala Asp Val Cys Met Asp Pro Glu Pro Ile Val Arg Ile Val
    280                 285                 290

ggt cga aat ggt cta tgt gtt gat gtt agg gat gga aga ttc cac 1037
Gly Arg Asn Gly Leu Cys Val Asp Val Arg Asp Gly Arg Phe His
    295                 300                 305

aac gga aac gca ata cag ttg tgg cca tgc aag tct aat aca gat 1082
Asn Gly Asn Ala Ile Gln Leu Trp Pro Cys Lys Ser Asn Thr Asp
    310                 315                 320

gca aat cag ctc tgg act ttg aaa aga gac aat act att cga tct 1127
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Ala Asn Gln Leu Trp Thr Leu Lys Arg Asp Asn Thr Ile Arg Ser
    325                 330                 335

aat gga aag tgt tta act act tac ggg tac agt ccg gga gtc tat 1172
Asn Gly Lys Cys Leu Thr Thr Tyr Gly Tyr Ser Pro Gly Val Tyr
    340                 345                 350

gtg atg atc tat gat tgc aat act gct gca act gat gcc acc cgc 1217
Val Met Ile Tyr Asp Cys Asn Thr Ala Ala Thr Asp Ala Thr Arg
    355                 360                 365

tgg caa ata tgg gat aat gga acc atc ata aat ccc aga tct agt 1262
Trp Gln Ile Trp Asp Asn Gly Thr Ile Ile Asn Pro Arg Ser Ser
    370                 375                 380

cta gtt tta gca gcg aca tca ggg aac agt ggt acc aca ctt aca 1307
Leu Val Leu Ala Ala Thr Ser Gly Asn Ser Gly Thr Thr Leu Thr
    385                 390                 395

gtg caa acc aac att tat gcc gtt agt caa ggt tgg ctt cct act 1352
Val Gln Thr Asn Ile Tyr Ala Val Ser Gln Gly Trp Leu Pro Thr
    400                 405                 410

aat aat aca caa cct ttt gtg aca acc att gtt ggg cta tat ggt 1397
Asn Asn Thr Gln Pro Phe Val Thr Thr Ile Val Gly Leu Tyr Gly
    415                 420                 425

ctg tgc ttg caa gca aat agt gga caa gta tgg ata gag gac tgt 1442
Leu Cys Leu Gln Ala Asn Ser Gly Gln Val Trp Ile Glu Asp Cys
    430                 435                 440

agc agt gaa aag gct gaa caa cag tgg gct ctt tat gca gat ggt 1487
Ser Ser Glu Lys Ala Glu Gln Gln Trp Ala Leu Tyr Ala Asp Gly
    445                 450                 455

tca ata cgt cct cag caa aac cga gat aat tgc ctt aca agt gat 1532
Ser Ile Arg Pro Gln Gln Asn Arg Asp Asn Cys Leu Thr Ser Asp
    460                 465                 470

tct aat ata cgg gaa aca gtt gtc aag atc ctc tct tgt ggc cct 1577
Ser Asn Ile Arg Glu Thr Val Val Lys Ile Leu Ser Cys Gly Pro
    475                 480                 485

gca tcc tct ggc caa cga tgg atg ttc aag aat gat gga acc att 1622
Ala Ser Ser Gly Gln Arg Trp Met Phe Lys Asn Asp Gly Thr Ile
    490                 495                 500

tta aat ttg tat agt ggg ttg gtg tta gat gtg agg gca tcg gat 1667
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Leu Asn Leu Tyr Ser Gly Leu Val Leu Asp Val Arg Ala Ser Asp
505 510 515

ccg agc ctt aaa caa atc att ctt tac cct ctc cat ggt gac cca 1712
Pro Ser Leu Lys Gln Ile Ile Leu Tyr Pro Leu His Gly Asp Pro
520 525 530

aac caa ata tgg tta cca tta ttt tgatagacag attactctct 1756
Asn Gln Ile Trp Leu Pro Leu Phe
535 540

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1 5 10

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<213> Human immunodeficiency virus

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1 5 10

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<211> 12

<212> PRT

<213> Ricinus communis

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Val Ser Ile Leu Ile Pro Ile Ile Ala Leu Met Val
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<210> 15

<211> 5

<212> PRT

<213> Rous sarcoma virus

<400> 15

Pro Pro Pro Pro Thr
1 5

<210> 16

<211> 4

<212> PRT

<213> Homo sapiens

<400> 16

Lys Asp Glu Leu
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<210> 17

<211> 5

<212> PRT

<213> Human immunodeficiency virus

<400> 17

Gly Ala Arg Ala Ser
1 5